

SEQUENCE LISTING

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Bouckaert, Julie

<120> Mutant Proteins, High Potency Inhibitory Antibodies, and FimCH Crystal Structure

<130> 10271-037

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<170> PatentIn version 3.0

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tgc ttg ctg gca ggt atc ctg atg ttc atg gca atg atg gtt gcc gga 96
 Cys Leu Leu Ala Gly Ile Leu Met Phe Met Ala Met Met Val Ala Gly
 20 25 30

cgc gct gaa gcg gga gtg gcc tta ggt gcg act cgc gta att tat ccg 144
 Arg Ala Glu Ala Gly Val Ala Leu Gly Ala Thr Arg Val Ile Tyr Pro
 35 40 45

gca ggg caa aaa caa gtg caa ctt gcc gtg aca aat aat gat gaa aat 192
 Ala Gly Gln Lys Gln Val Gln Leu Ala Val Thr Asn Asn Asp Glu Asn
 50 55 60

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agt acc tat tta att caa tca tgg gtg gaa aat gcc gat ggt gta aag      240
Ser Thr Tyr Leu Ile Gln Ser Trp Val Glu Asn Ala Asp Gly Val Lys
   65          70          75          80

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gat ggt cgt ttt atc gtg acg cct cct ctg ttt gcg atg aag gga aaa 288
Asp Gly Arg Phe Ile Val Thr Pro Pro Leu Phe Ala Met Lys Gly Lys
85 90 95

aaa gag aat acc tta cgt att ctt gat gca aca aat aac caa ttg cca 336
 Lys Glu Asn Thr Leu Arg Ile Leu Asp Ala Thr Asn Asn Gln Leu Pro
 100 105 110

cag gac cg^g gaa agt tta ttc tgg atg aac gtt aaa gc^g att ccg tca 384
 Gln Asp Arg Glu Ser Leu Phe Trp Met Asn Val Lys Ala Ile Pro Ser
 115 120 125

atg gat aaa tca aaa ttg act gag aat acg cta cag ctc gca att atc 432
 Met Asp Lys Ser Lys Leu Thr Glu Asn Thr Leu Gln Leu Ala Ile Ile
 130 135 140

agc cgc att aaa ctg tac tat cgc ccg gct aaa tta gcg ttg cca ccc 480
 Ser Arg Ile Lys Leu Tyr Tyr Arg Pro Ala Lys Leu Ala Leu Pro Pro
 145 150 155 160

gat cag gcc gca gaa aaa tta aga ttt cgt cgt agc gcg aat tct ctg 528
 Asp Gln Ala Ala Glu Lys Leu Arg Phe Arg Arg Ser Ala Asn Ser Leu
 165 170 175

acg ctg att aac ccg aca ccc tat tac ctg acg gta aca gag ttg aat 576
 Thr Leu Ile Asn Pro Thr Pro Tyr Tyr Leu Thr Val Thr Glu Leu Asn
 180 185 190

gcc gga acc cgg gtt ctt gaa aat gca ttg gtg cct cca atg ggc gaa 624
 Ala Gly Thr Arg Val Leu Glu Asn Ala Leu Val Pro Pro Met Gly Glu
 195 200 205

agc acg gtt aaa ttg cct tct gat gca gga agc aat att act tac cga 672
 Ser Thr Val Lys Leu Pro Ser Asp Ala Gly Ser Asn Ile Thr Tyr Arg
 210 215 220

aca ata aat gat tat ggc gca ctt acc ccc aaa atg acg ggc gta atg 720
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gaa taa 726
 Glu

<210> 2
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 <213> E. coli

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 35 40 45
 Ala Gly Gln Lys Gln Val Gln Leu Ala Val Thr Asn Asn Asp Glu Asn
 50 55 60
 Ser Thr Tyr Leu Ile Gln Ser Trp Val Glu Asn Ala Asp Gly Val Lys
 65 70 75 80
 Asp Gly Arg Phe Ile Val Thr Pro Pro Leu Phe Ala Met Lys Gly Lys
 85 90 95
 Lys Glu Asn Thr Leu Arg Ile Leu Asp Ala Thr Asn Asn Gln Leu Pro
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 Gln Asp Arg Glu Ser Leu Phe Trp Met Asn Val Lys Ala Ile Pro Ser
 115 120 125
 Met Asp Lys Ser Lys Leu Thr Glu Asn Thr Leu Gln Leu Ala Ile Ile
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 Ser Arg Ile Lys Leu Tyr Tyr Arg Pro Ala Lys Leu Ala Leu Pro Pro
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gta aat gcc tgg tca ttc gcc tgt aaa acc gcc aat ggt acc gct atc      96
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cct att ggc ggt ggc agc gcc aat gtt tat gta aac ctt gcg ccc gtc
 Pro Ile Gly Gly Ser Ala Asn Val Tyr Val Asn Leu Ala Pro Val
 15 20 25

tgc cat aac gat tat ccg gaa acc att aca gac tat gtc aca ctg caa
 Cys His Asn Asp Tyr Pro Glu Thr Ile Thr Asp Tyr Val Thr Leu Gln
 45 50 55

cga ggc tcg gct tat ggc ggc gtg tta tct aat ttt tcc ggg acc gta
 Arg Gly Ser Ala Tyr Gly Gly Val Leu Ser Asn Phe Ser Gly Thr Val
 60 65 70 75

aaa tat agt ggc agt agc tat cca ttt cct acc acc acc agc gaa acg ccg
Lys Tyr Ser Gly Ser Ser Tyr Pro Phe Pro Thr Thr Ser Glu Thr Pro
80 85 90

cgc gtt gtt tat aat tcg aga acg gat aag ccg tgg ccg gtg gcg ctt 384
 Arg Val Val Tyr Asn Ser Arg Thr Asp Lys Pro Trp Pro Val Ala Leu
 95 100 105

tat ttg acg cct gtg agc agt gcg ggc ggg gtg gcg att aaa gct ggc 432
 Tyr Leu Thr Pro Val Ser Ser Ala Gly Gly Val Ala Ile Lys Ala Gly
 110 115 120

tca tta att gcc gtg ctt att ttg cga cag acc aac aac tat aac agc	480
Ser Leu Ile Ala Val Leu Ile Leu Arg Gln Thr Asn Asn Tyr Asn Ser	
125 130 135	

gat gat ttc cag ttt gtg tgg aat att tac gcc aat aat gat gtg gtg		528
Asp Asp Phe Gln Phe Val Trp Asn Ile Tyr Ala Asn Asn Asp Val Val		
140 145 150 155		
gtg cct act ggc ggc tgc gat gtt tct gct cgt gat gtc acc gtt act		576
Val Pro Thr Gly Gly Cys Asp Val Ser Ala Arg Asp Val Thr Val Thr		
160 165 170		
ctg ccg gac tac cct ggt tca gtg cca att cct ctt acc gtt tat tgt		624
Leu Pro Asp Tyr Pro Gly Ser Val Pro Ile Pro Leu Thr Val Tyr Cys		
175 180 185		
gcg aaa agc caa aac ctg ggg tat tac ctc tcc ggc aca acc gca gat		672
Ala Lys Ser Gln Asn Leu Gly Tyr Tyr Leu Ser Gly Thr Thr Ala Asp		
190 195 200		
gcg ggc aac tcg att ttc acc aat acc gcg tcg ttt tca cct gca cag		720
Ala Gly Asn Ser Ile Phe Thr Asn Thr Ala Ser Phe Ser Pro Ala Gln		
205 210 215		
ggc gtc ggc gta cag ttg acg cgc aac ggt acg att att cca gcg aat		768
Gly Val Gly Val Gln Leu Thr Arg Asn Gly Thr Ile Ile Pro Ala Asn		
220 225 230 235		
aac acg gta tcg tta gga gca gta ggg act tcg gcg gtg agt ctg gga		816
Asn Thr Val Ser Leu Gly Ala Val Gly Thr Ser Ala Val Ser Leu Gly		
240 245 250		
tta acg gca aat tat gca cgt acc gga ggg cag gtg act gca ggg aat		864
Leu Thr Ala Asn Tyr Ala Arg Thr Gly Gly Gln Val Thr Ala Gly Asn		
255 260 265		
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270 275		

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Pro Ile Gly Gly Ser Ala Asn Val Tyr Val Asn Leu Ala Pro Val		
15 20 25		
Val Asn Val Gly Gln Asn Leu Val Val Asp Leu Ser Thr Gln Ile Phe		
30 35 40		
Cys His Asn Asp Tyr Pro Glu Thr Ile Thr Asp Tyr Val Thr Leu Gln		
45 50 55		
Arg Gly Ser Ala Tyr Gly Gly Val Leu Ser Asn Phe Ser Gly Thr Val		
60 65 70 75		
Lys Tyr Ser Gly Ser Ser Tyr Pro Phe Pro Thr Thr Ser Glu Thr Pro		
80 85 90		
Arg Val Val Tyr Asn Ser Arg Thr Asp Lys Pro Trp Pro Val Ala Leu		
95 100 105		
Tyr Leu Thr Pro Val Ser Ser Ala Gly Gly Val Ala Ile Lys Ala Gly		
110 115 120		

Ser Leu Ile Ala Val Leu Ile Leu Arg Gln Thr Asn Asn Tyr Asn Ser
125 130 135
Asp Asp Phe Gln Phe Val Trp Asn Ile Tyr Ala Asn Asn Asp Val Val
140 145 150 155
Val Pro Thr Gly Gly Cys Asp Val Ser Ala Arg Asp Val Thr Val Thr
160 165 170
Leu Pro Asp Tyr Pro Gly Ser Val Pro Ile Pro Leu Thr Val Tyr Cys
175 180 185
Ala Lys Ser Gln Asn Leu Gly Tyr Tyr Leu Ser Gly Thr Thr Ala Asp
190 195 200
Ala Gly Asn Ser Ile Phe Thr Asn Thr Ala Ser Phe Ser Pro Ala Gln
205 210 215
Gly Val Gly Val Gln Leu Thr Arg Asn Gly Thr Ile Ile Pro Ala Asn
220 225 230 235
Asn Thr Val Ser Leu Gly Ala Val Gly Thr Ser Ala Val Ser Leu Gly
240 245 250
Leu Thr Ala Asn Tyr Ala Arg Thr Gly Gly Gln Val Thr Ala Gly Asn
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Val Gln Ser Ile Ile Gly Val Thr Phe Val Tyr Gln
270 275

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<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

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<210> 6
<211> 28
<212> DNA
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<210> 7
<211> 48
<212> DNA
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48

<210> 8
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<212> DNA
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<212> DNA
<213> Artificial

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<210> 11
<211> 44
<212> DNA
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<210> 13
<211> 24
<212> DNA
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<220>
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accattacaa actatgtcac actg 24

<210> 24
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<220>
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<210> 25
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<210> 41
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卷之三

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<210> 43
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<212> DNA
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<220>
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<210> 44
<211> 22
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<220>
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<400> 44
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<210> 45
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<220>
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<210> 46
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<220>
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<210> 47
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<400> 47
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<210> 48
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<220>
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<400> 48
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<210> 49
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<210> 50
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